

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/528,684
Source: PCR
Date Processed by STIC: 1/31/06

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 01/31/2006

PATENT APPLICATION: US/10/528,684

TIME: 16:15:04

Input Set : A:\211010031U3.txt

Output Set: N:\CRF4\01312006\J528684.raw

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4 <110> APPLICANT: Fleckenstein, Annette E.
5      Hanson, Glen R.
7 <120> TITLE OF INVENTION: MODULATING VESICULAR MONOAMINE TRANSPORTER
8      TRAFFICKING AND FUNCTION: A NOVEL APPROACH FOR
9      THE TREATMENT OF PARKINSON'S DISEASE
11 <130> FILE REFERENCE: 21101.0031U3
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/528,684
C--> 13 <141> CURRENT FILING DATE: 2005-03-21
13 <150> PRIOR APPLICATION NUMBER: PCT/US03/29668
14 <151> PRIOR FILING DATE: 2003-09-19
16 <150> PRIOR APPLICATION NUMBER: 60/412,439
17 <151> PRIOR FILING DATE: 2002-09-19
19 <160> NUMBER OF SEQ ID NOS: 18
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 515
25 <212> TYPE: PRT
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
30      synthetic construct
32 <400> SEQUENCE: 1
33 Met Ala Leu Ser Asp Leu Val Leu Leu Arg Trp Leu Arg Asp Ser Arg
34 1          5          10          15
35 His Ser Arg Lys Leu Ile Leu Phe Ile Val Phe Leu Ala Leu Leu Leu
36          20          25          30
37 Asp Asn Met Leu Leu Thr Val Val Val Pro Ile Ile Pro Ser Tyr Leu
38          35          40          45
39 Tyr Ser Ile Lys His Glu Lys Asn Ser Thr Glu Ile Gln Thr Thr Arg
40          50          55          60
41 Pro Glu Leu Val Val Ser Thr Ser Glu Ser Ile Phe Ser Tyr Tyr Asn
42 65          70          75          80
43 Asn Ser Thr Val Leu Ile Thr Gly Asn Ala Thr Gly Thr Leu Pro Gly
44          85          90          95
45 Gly Gln Ser His Lys Ala Thr Ser Thr Gln His Thr Val Ala Asn Thr
46          100         105         110
47 Thr Val Pro Ser Asp Cys Pro Ser Glu Asp Arg Asp Leu Leu Asn Glu
48          115         120         125
49 Asn Val Gln Val Gly Leu Leu Phe Ala Ser Lys Ala Thr Val Gln Leu
50          130         135         140
51 Leu Thr Asn Pro Phe Ile Gly Leu Leu Thr Asn Arg Ile Gly Tyr Pro
52 145         150         155         160
53 Ile Pro Met Phe Ala Gly Phe Cys Ile Met Phe Ile Ser Thr Val Met

```

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54          165          170          175
55 Phe Ala Phe Ser Ser Ser Tyr Ala Phe Leu Leu Ile Ala Arg Ser Leu
56          180          185          190
57 Gln Gly Ile Gly Ser Ser Cys Ser Ser Val Ala Gly Met Gly Met Leu
58          195          200          205
59 Ala Ser Val Tyr Thr Asp Asp Glu Glu Arg Gly Asn Ala Met Gly Ile
60          210          215          220
61 Ala Leu Gly Gly Leu Ala Met Gly Val Leu Val Gly Pro Pro Phe Gly
62 225          230          235          240
63 Ser Val Leu Tyr Glu Phe Val Gly Lys Thr Ala Pro Phe Leu Val Leu
64          245          250          255
65 Ala Ala Leu Val Leu Leu Asp Gly Ala Ile Gln Leu Phe Val Leu Gln
66          260          265          270
67 Pro Ser Arg Val Gln Pro Glu Ser Gln Lys Gly Thr Pro Leu Thr Thr
68          275          280          285
69 Leu Leu Lys Asp Pro Tyr Ile Leu Ile Ala Ala Gly Ser Ile Cys Phe
70          290          295          300
71 Ala Asn Met Gly Ile Ala Met Leu Glu Pro Ala Leu Pro Ile Trp Met
72 305          310          315          320
73 Met Glu Thr Met Cys Ser Arg Lys Trp Gln Leu Gly Val Ala Phe Leu
74          325          330          335
75 Pro Ala Ser Ile Ser Tyr Leu Ile Gly Thr Asn Ile Phe Gly Ile Leu
76          340          345          350
77 Ala His Lys Met Gly Arg Trp Leu Cys Ala Leu Leu Gly Met Val Ile
78          355          360          365
79 Val Gly Ile Ser Ile Leu Cys Ile Pro Phe Ala Lys Asn Ile Tyr Gly
80          370          375          380
81 Leu Ile Ala Pro Asn Phe Gly Val Gly Phe Ala Ile Gly Met Val Asp
82 385          390          395          400
83 Ser Ser Met Met Pro Ile Met Gly Tyr Leu Val Asp Leu Arg His Val
84          405          410          415
85 Ser Val Tyr Gly Ser Val Tyr Ala Ile Ala Asp Val Ala Phe Cys Met
86          420          425          430
87 Gly Tyr Ala Ile Gly Pro Ser Ala Gly Gly Ala Ile Ala Lys Ala Ile
88          435          440          445
89 Gly Phe Pro Trp Leu Met Thr Ile Ile Gly Ile Ile Asp Ile Ala Phe
90          450          455          460
91 Ala Pro Leu Cys Phe Phe Leu Arg Ser Pro Pro Ala Lys Glu Glu Lys
92 465          470          475          480
93 Met Ala Ile Leu Met Asp His Asn Cys Pro Ile Lys Thr Lys Met Tyr
94          485          490          495
95 Thr Gln Asn Asn Val Gln Ser Tyr Pro Ile Gly Asp Asp Glu Glu Ser
96          500          505          510
97 Glu Ser Asp
98          515
100 <210> SEQ ID NO: 2
101 <211> LENGTH: 1548
102 <212> TYPE: DNA
103 <213> ORGANISM: Artificial Sequence

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105 <220> FEATURE:

106 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
107 synthetic construct

109 <400> SEQUENCE: 2

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110 atggccctga gcatctggt gctgctgca tggctgcggg acagccgcca ctgcgcgaaa      60
111 ctgacccgtg tcatcggtgt ccttgccgtg ctgctggaca acatgctgct caccgtcgtg      120
112 gttcccatca tcccagcta tctgtacagc attaagcatg agaaaaactc tacggaaatc      180
113 cagaccacca gaccagagct cgtggtctcc acctccgaaa gcatcttctc ttactataac      240
114 aactctactg tgttgatcac cgggaatgcc actgggactc ttccaggagg gcagtccacac      300
115 aaggctacca gcacacagca cactgtggct aacaccactg tcccttcgga ctgtcccagt      360
116 gaagacagag accttctgaa tgagaatgtg caagttgggc tgcgttttgc ctccaaagcc      420
117 actgtccagc tcctcactaa cccattcata ggacttctga ccaacagaat tggctatcca      480
118 attcccatgt ttgccggctt ctgcatcatg tttatctcaa cagttatgtt tgccttctcc      540
119 agcagctatg ccttcctgct gatcgccagg tcccttcagg gaattggctc ctctgctca      600
120 tccgtggctg ggatgggtat gctggccagc gtgtacacag atgatgagga gagggggaac      660
121 gccatgggca ttgctttggg tggcctggcc atgggagctc tagtgggacc ccccttcggg      720
122 agtgtgctct atgagtttgt ggggaagaca gctcccttcc tgggtgctagc tgccttgggtg      780
123 ctcttggatg gggctattca gctctttgtg ctccagccgt cccgagtaca gccagagagt      840
124 cagaagggga cacctctaac gaccttgctg aaggatccat acatcctcat cgctgcaggc      900
125 tccatctgct ttgcaaacat ggggatagcc atgctggagc ccgccctgcc catctggatg      960
126 atggagacca tgtgttcccg aaagtggcag ctgggcgttg ctttcctccc ggcgagcatc     1020
127 tcttatctca ttggaaccaa tatttttggg atacttgcac acaaaatggg aaggtggcta     1080
128 tgtgctcttc tgggaatggt aattgttggg atcagcattt tatgcatccc ctttgcaaaa     1140
129 aatatctatg gactcatcgc tcccaacttt ggagttgggt ttgcaattgg gatggtggac     1200
130 tcctctatga tgccatcatc gggctacctg gttgacctgc ggcattgtgc tgtctatggg     1260
131 agtgtttatg ccattgcaga cgtggccttt tgtatgggct atgctatcgg tccctctgct     1320
132 ggtgggtgcca tcgcaaaggc aattggcttt ccttggctta tgacaattat tgggataatt     1380
133 gatatcgctt ttgctccact ctgctttttc cttcgaagtc cacctgctaa ggaggaaaaa     1440
134 atggctatcc tcatggacca caactgtccc attaaaacaa agatgtacac tcagaataat     1500
135 gtccagtcac atcccacggt tgatgatgaa gaatctgaaa gtgactga      1548

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137 <210> SEQ ID NO: 3

138 <211> LENGTH: 514

139 <212> TYPE: PRT

140 <213> ORGANISM: Artificial Sequence

142 <220> FEATURE:

143 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
144 synthetic construct

146 <400> SEQUENCE: 3

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147 Met Ala Leu Ser Glu Leu Ala Leu Val Arg Trp Leu Gln Glu Ser Arg
148 1          5          10          15
149 His Ser Arg Lys Leu Ile Leu Phe Ile Val Phe Leu Ala Leu Leu Leu
150          20          25          30
151 Asp Asn Met Leu Leu Thr Val Val Val Pro Ile Ile Pro Ser Tyr Leu
152          35          40          45
153 Tyr Ser Ile Lys His Glu Lys Asn Ala Thr Glu Ile Gln Thr Ala Arg
154          50          55          60
155 Pro Val His Thr Ala Ser Ile Ser Asp Ser Phe Gln Ser Ile Phe Ser
156 65          70          75          80
157 Tyr Tyr Asp Asn Ser Thr Met Val Thr Gly Asn Ala Thr Arg Asp Leu

```

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158				85				90				95	
159	Thr	Leu	His	Gln	Thr	Ala	Thr	Gln	His	Met	Val	Thr	Asn
160				100				105				110	
161	Val	Pro	Ser	Asp	Cys	Pro	Ser	Glu	Asp	Lys	Asp	Leu	Leu
162				115				120				125	
163	Val	Gln	Val	Gly	Leu	Leu	Phe	Ala	Ser	Lys	Ala	Thr	Val
164				130				135				140	
165	Thr	Asn	Pro	Phe	Ile	Gly	Leu	Leu	Thr	Asn	Arg	Ile	Gly
166	145					150					155		160
167	Pro	Ile	Phe	Ala	Gly	Phe	Cys	Ile	Met	Phe	Val	Ser	Thr
168					165					170			175
169	Ala	Phe	Ser	Ser	Ser	Tyr	Ala	Phe	Leu	Leu	Ile	Ala	Arg
170					180					185			190
171	Gly	Ile	Gly	Ser	Ser	Cys	Ser	Ser	Val	Ala	Gly	Met	Gly
172					195					200			205
173	Ser	Val	Tyr	Thr	Asp	Asp	Glu	Glu	Arg	Gly	Asn	Val	Met
174					210					215			220
175	Leu	Gly	Gly	Leu	Ala	Met	Gly	Val	Leu	Val	Gly	Pro	Pro
176	225					230					235		240
177	Val	Leu	Tyr	Glu	Phe	Val	Gly	Lys	Thr	Ala	Pro	Phe	Leu
178					245					250			255
179	Ala	Leu	Val	Leu	Leu	Asp	Gly	Ala	Ile	Gln	Leu	Phe	Val
180					260					265			270
181	Ser	Arg	Val	Gln	Pro	Glu	Ser	Gln	Lys	Gly	Thr	Pro	Leu
182					275					280			285
183	Leu	Lys	Asp	Pro	Tyr	Ile	Leu	Ile	Ala	Ala	Gly	Ser	Ile
184					290					295			300
185	Asn	Met	Gly	Ile	Ala	Met	Leu	Glu	Pro	Ala	Leu	Pro	Ile
186	305					310					315		320
187	Glu	Thr	Met	Cys	Ser	Arg	Lys	Trp	Gln	Leu	Gly	Val	Ala
188					325					330			335
189	Ala	Ser	Ile	Ser	Tyr	Leu	Ile	Gly	Thr	Asn	Ile	Phe	Gly
190					340					345			350
191	His	Lys	Met	Gly	Arg	Trp	Leu	Cys	Ala	Leu	Leu	Gly	Met
192					355					360			365
193	Gly	Val	Ser	Ile	Leu	Cys	Ile	Pro	Phe	Ala	Lys	Asn	Ile
194					370					375			380
195	Ile	Ala	Pro	Asn	Phe	Gly	Val	Gly	Phe	Ala	Ile	Gly	Met
196	385					390					395		400
197	Ser	Met	Met	Pro	Ile	Met	Gly	Tyr	Leu	Val	Asp	Leu	Arg
198					405					410			415
199	Val	Tyr	Gly	Ser	Val	Tyr	Ala	Ile	Ala	Asp	Val	Ala	Phe
200					420					425			430
201	Tyr	Ala	Ile	Gly	Pro	Ser	Ala	Gly	Gly	Ala	Ile	Ala	Lys
202					435					440			445
203	Phe	Pro	Trp	Leu	Met	Thr	Ile	Ile	Gly	Ile	Ile	Asp	Ile
204					450					455			460
205	Pro	Leu	Cys	Phe	Phe	Leu	Arg	Ser	Pro	Pro	Ala	Lys	Glu
206	465					470				475			480

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```

207 Ala Ile Leu Met Asp His Asn Cys Pro Ile Lys Thr Lys Met Tyr Thr
208                               485                               490                               495
209 Gln Asn Asn Ile Gln Ser Tyr Pro Ile Gly Glu Asp Glu Glu Ser Glu
210                               500                               505                               510
211 Ser Asp
214 <210> SEQ ID NO: 4
215 <211> LENGTH: 1545
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
221     synthetic construct
223 <400> SEQUENCE: 4
224 atggccctga gcgagctggc gctgggtccgc tggctgcagg agagccgcca ctcgcggaag      60
225 ctcctcctgt tcctcgtgtt cctggcgctg ctgctggaca acatgctgct cactgtcgtg      120
226 gtcccatca tcccaagtta tctgtacagc attaagcatg agaagaatgc tacagaaatc      180
227 cagacggcca ggccagtga cactgcctcc atctcagaca gcttccagag catcttctcc      240
228 tattatgata actcgactat ggtcaccggg aatgctacca gagacctgac acttcatcag      300
229 accgccacac agcacatggg gaccaacgcg tccgctgttc cttccgactg tcccagtgaa      360
230 gacaaagacc tcctgaatga aaacgtgcaa gttggctctgt tgtttgcctc gaaagccacc      420
231 gtccagctca tcaccaaccc ttctcatagga ctactgacca acagaattgg ctatccaatt      480
232 cccatatttg cgggattctg catcatgttt gtctcaacaa ttatgtttgc cttctccagc      540
233 agctatgcct tcctgctgat tgccaggtcg ctgcagggca tcggctcgtc ctgctcctct      600
234 gtggctggga tgggcatgct tgccagtgtc tacacagatg atgaagagag aggcaacgtc      660
235 atgggaatcg ccttgggagg cctggccatg ggggtcttag tgggcccccc cttcgggagt      720
236 gtgctctatg agtttgtggg gaagacggct ccgttcctgg tgctggccgc cctggtactc      780
237 ttggatggag ctattcagct ctttgtgctc cagccgtccc ggggtgcagcc agagagtcag      840
238 aaggggacac ccctaaccac gctgctgaag gacccgtaca tcctcattgc tgcaggctcc      900
239 atctgctttg caaacatggg catcgccatg ctggagccag ccctgcccac ctggatgatg      960
240 gagaccatgt gttcccgaag gtggcagctg ggcgttgccct tcttgccagc tagtatctct      1020
241 tatctcattg gaaccaatat ttttgggata cttgcacaca aaatggggag gtggctttgt      1080
242 gctcttctgg gaatgataat tgttggagtc agcattttat gtattccatt tgcaaaaaac      1140
243 atttatggac tcatagctcc gaactttgga gttggttttg caattggaat ggtggattcg      1200
244 tcaatgatgc ctatcatggg ctacctcgta gacctgcggc acgtgtccgt ctatgggagt      1260
245 gtgtacgcca ttgcggatgt ggcattttgt atggggtatg ctataggtcc ttctgctggt      1320
246 ggtgctattg caaaggcaat tggatttcca tggctcatga caattattgg gataattgat      1380
247 attctttttg cccctctctg cttttttctt cgaagtccac ctgccaaaga agaaaaaatg      1440
248 gctattctca tggatcacia ctgccctatt aaaacaaaaa tgtacactca gaataatatc      1500
249 cagtcatatc cgatagggtga agatgaagaa tctgaaagtg actga      1545
251 <210> SEQ ID NO: 5
252 <211> LENGTH: 525
253 <212> TYPE: PRT
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
258     synthetic construct
260 <400> SEQUENCE: 5
261 Met Leu Arg Thr Ile Leu Asp Ala Pro Gln Arg Leu Leu Lys Glu Gly
262 1                               5                               10                               15

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VERIFICATION SUMMARY

DATE: 01/31/2006

PATENT APPLICATION: US/10/528,684

TIME: 16:15:05

Input Set : A:\211010031U3.txt

Output Set: N:\CRF4\01312006\J528684.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date